

030

RAW SEQUENCE LISTING

ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

ST 1.5

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/543,679

Art Unit / Team No. :

O/PE

Date Processed by STIC:

4/25/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/543,679</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

INPUT SET: S35381.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

**Does Not Comply
Corrected Diskette Needed**

SEQUENCE LISTING

3 (1) General Information
 4 (i) APPLICANT: East Carolina University
 5 et al.
 6 (ii) TITLE OF THE INVENTION: LOW ADENOSINE
 7 OLIGONUCLEOTIDE AGENT,
 8
 9 TREATMENTS
 10 (iii) NUMBER OF SEQUENCES: 3110
 11 (iv) CORRESPONDENCE ADDRESS:
 12 (A) ADDRESSEE: ARTER & HADDEN
 13 (B) STREET: 725 South Figueroa St, #
 14 3400
 15 (C) CITY: Los Angeles
 16 (D) STATE: CA
 17 (E) COUNTRY: USA
 18 (F) ZIP: 90071
 19 (v) COMPUTER READABLE FORM:
 20 (A) MEDIUM TYPE: Diskette
 21 (B) COMPUTER: IBM Compatible
 22 (C) OPERATING SYSTEM: DOS
 23 (D) SOFTWARE: FastSEQ for Windows
 24 Version 2.0
 25 (vi) CURRENT APPLICATION DATA:
 26 (A) APPLICATION NUMBER: PCT/US99/
 27 (B) FILING DATE: 3-AUG-1999
 28 (C) CLASSIFICATION: UNKNOWN
 29 (vii) PRIOR APPLICATION DATA:
 30 (A) APPLICATION NUMBER: 60/095,212
 31 (B) FILING DATE: 03-AUG-1998
 32 (viii) ATTORNEY/AGENT INFORMATION:
 33 (A) NAME: Amzel, Viviana
 34 (B) REGISTRATION NUMBER: 30,930
 35 (C) REFERENCE/DOCKET NUMBER: EPI-109
 36 (ix) TELECOMMUNICATION INFORMATION:
 37 (A) TELEPHONE: 213-430-3520
 38 (B) TELEFAX: 213-617-9255
 39 (C) TELEX:
 40

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:25:58

INPUT SET: S35381.raw

41 (2) INFORMATION FOR SEQ ID NO:1:
42 (i) SEQUENCE CHARACTERISTICS:
--> 43 (A) LENGTH: 21 base pairs
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear
47 (ii) MOLECULE TYPE: cDNA
48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
49 GATGGAGGGC GGCATGGCGG G
50 21
51

global
format error
→ 21

52 (2) INFORMATION FOR SEQ ID NO:2:
53 (i) SEQUENCE CHARACTERISTICS:
--> 54 (A) LENGTH: 21 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58 (ii) MOLECULE TYPE: cDNA
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
60 GTAGCAGGCG GGGATGGGG C
61 21
62

same error

63 (2) INFORMATION FOR SEQ ID NO:3:
64 (i) SEQUENCE CHARACTERISTICS:
--> 65 (A) LENGTH: 18 base pairs
66 (B) TYPE: nucleic acid
67 (C) STRANDEDNESS: single
68 (D) TOPOLOGY: linear
69 (ii) MOLECULE TYPE: cDNA
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
71 GTTGTGGGC ATCTTGCC
72 18
73

same

74 (2) INFORMATION FOR SEQ ID NO:4:
75 (i) SEQUENCE CHARACTERISTICS:
--> 76 (A) LENGTH: 18 base pairs
77 (B) TYPE: nucleic acid
78 (C) STRANDEDNESS: single
79 (D) TOPOLOGY: linear
80 (ii) MOLECULE TYPE: cDNA
81 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
82 GTACTTGCGG ATCTAGGC
83 18
84

same

85 (2) INFORMATION FOR SEQ ID NO:5:
86 (i) SEQUENCE CHARACTERISTICS:
--> 87 (A) LENGTH: 18 base pairs
88 (B) TYPE: nucleic acid
89 (C) STRANDEDNESS: single

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PATENT APPLICATION US/09/543,679DATE: 04/25/2000
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90 (D) TOPOLOGY: linear
91 (ii) MOLECULE TYPE: cDNA
92 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
93 GTGGGCCTAG CTCTCGCC
94 18
95

Same

96 (2) INFORMATION FOR SEQ ID NO:6:
97 (i) SEQUENCE CHARACTERISTICS:
--> 98 (A) LENGTH: 18 base pairs
99 (B) TYPE: nucleic acid
100 (C) STRANDEDNESS: single
101 (D) TOPOLOGY: linear
102 (ii) MOLECULE TYPE: cDNA
103 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
104 GTCGGGGTAC CTGTCGGC
105 18
106

107 (2) INFORMATION FOR SEQ ID NO:7:
108 (i) SEQUENCE CHARACTERISTICS:
--> 109 (A) LENGTH: 21 base pairs
110 (B) TYPE: nucleic acid
111 (C) STRANDEDNESS: single
112 (D) TOPOLOGY: linear
113 (ii) MOLECULE TYPE: cDNA
114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
115 CTCGTCGCCG TCGCCGGCG G
116 21
117

118 (2) INFORMATION FOR SEQ ID NO:8:
119 (i) SEQUENCE CHARACTERISTICS:
--> 120 (A) LENGTH: 20 base pairs
121 (B) TYPE: nucleic acid
122 (C) STRANDEDNESS: single
123 (D) TOPOLOGY: linear
124 (ii) MOLECULE TYPE: cDNA
125 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
126 GGGTGGTGCT ATTGTGGGC
127 20
128

129 (2) INFORMATION FOR SEQ ID NO:9:
130 (i) SEQUENCE CHARACTERISTICS:
--> 131 (A) LENGTH: 15 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: single
134 (D) TOPOLOGY: linear
135 (ii) MOLECULE TYPE: cDNA
136 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
137 GGCCCAGGGC CAGCC
138 15

✓

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TIME: 12:25:59

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139

140 (2) INFORMATION FOR SEQ ID NO:10:
141 (i) SEQUENCE CHARACTERISTICS:
--> 142 (A) LENGTH: 21 base pairs
143 (B) TYPE: nucleic acid
144 (C) STRANDEDNESS: single
145 (D) TOPOLOGY: linear
146 (ii) MOLECULE TYPE: cDNA
147 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
148 GCCCGGGCCA GCCGGGCCCC G
149 21
150

Same

151 (2) INFORMATION FOR SEQ ID NO:11:
152 (i) SEQUENCE CHARACTERISTICS:
--> 153 (A) LENGTH: 50 base pairs
154 (B) TYPE: nucleic acid
155 (C) STRANDEDNESS: single
156 (D) TOPOLOGY: linear
157 (ii) MOLECULE TYPE: cDNA
158 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
159 GCGGCCTGGAA AAGCTGAGAT GGAGGGCGGC ATGGCAGGCA CAGGCTGGC
160 50
161

162 (2) INFORMATION FOR SEQ ID NO:12:
163 (i) SEQUENCE CHARACTERISTICS:
--> 164 (A) LENGTH: 49 base pairs
165 (B) TYPE: nucleic acid
166 (C) STRANDEDNESS: single
167 (D) TOPOLOGY: linear
168 (ii) MOLECULE TYPE: cDNA
169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
170 CGGCCTGGAA AGCTGAGATG GAGGGCGGC ACAGGCTGGC
171 49
172

173 (2) INFORMATION FOR SEQ ID NO:13:
174 (i) SEQUENCE CHARACTERISTICS:
--> 175 (A) LENGTH: 48 base pairs
176 (B) TYPE: nucleic acid
177 (C) STRANDEDNESS: single
178 (D) TOPOLOGY: linear
179 (ii) MOLECULE TYPE: cDNA
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
181 GGCCTGGAAA GCTGAGATGG AGGGCGGCAT GGCGGGCAC AAGGCTGGC
182 48
183

184 (2) INFORMATION FOR SEQ ID NO:14:
185 (i) SEQUENCE CHARACTERISTICS:
--> 186 (A) LENGTH: 47 base pairs

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187 (B) TYPE: nucleic acid
 188 (C) STRANDEDNESS: single
 189 (D) TOPOLOGY: linear
 190 (ii) MOLECULE TYPE: cDNA
 191 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 192 GCCTGGAAAG CTGAGATGGA GGGCGGCATG CGGGCACAG GCTGGGC
 193 47
 194

Same

195 (2) INFORMATION FOR SEQ ID NO:15:
 196 (i) SEQUENCE CHARACTERISTICS:
 --> 197 (A) LENGTH: 46 base pairs
 198 (B) TYPE: nucleic acid
 199 (C) STRANDEDNESS: single
 200 (D) TOPOLOGY: linear
 201 (ii) MOLECULE TYPE: cDNA
 202 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 203 CCTGGAAAGC TGAGATGGAG GGGCGCATGG CGGGCACAGG CTGGGC
 204 46
 205

206 (2) INFORMATION FOR SEQ ID NO:16:
 207 (i) SEQUENCE CHARACTERISTICS:
 --> 208 (A) LENGTH: 45 base pairs
 209 (B) TYPE: nucleic acid
 210 (C) STRANDEDNESS: single
 211 (D) TOPOLOGY: linear
 212 (ii) MOLECULE TYPE: cDNA
 213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
 214 CTGGAAAGCT GAGATGGAGG GGGCATGGC GGGCACAGGC TGGGC
 215 45
 216

217 (2) INFORMATION FOR SEQ ID NO:17:
 218 (i) SEQUENCE CHARACTERISTICS:
 --> 219 (A) LENGTH: 44 base pairs
 220 (B) TYPE: nucleic acid
 221 (C) STRANDEDNESS: single
 222 (D) TOPOLOGY: linear
 223 (ii) MOLECULE TYPE: cDNA
 224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
 225 TGGAAAGCTG AGATGGAGGG CGGCATGGCG GGCACAGGCT GGGC
 226 44
 227

228 (2) INFORMATION FOR SEQ ID NO:18:
 229 (i) SEQUENCE CHARACTERISTICS:
 --> 230 (A) LENGTH: 43 base pairs
 231 (B) TYPE: nucleic acid
 232 (C) STRANDEDNESS: single
 233 (D) TOPOLOGY: linear
 234 (ii) MOLECULE TYPE: cDNA
 235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

*These errors
are global. See
Item 1 or
Error summary
sheet*

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:08

INPUT SET: S35381.raw

26157 8
26158

26159 (2) INFORMATION FOR SEQ ID NO:2420:
 26160 (i) SEQUENCE CHARACTERISTICS:
 --> 26161 (A) LENGTH: 981 base pairs
 26162 (B) TYPE: nucleic acid
 26163 (C) STRANDEDNESS: single
 26164 (D) TOPOLOGY: linear
 26165 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:
 26166 1 ATGCCGCCCT CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT
 26167 GCTCATGCC
 26168 61 CTGGTCTCTG TGCCCCGGAA CGTGCTGGTG ATCTGGCGGG TGAAGGTGAA
 26169 CCAGGGCGCTG
 26170 121 CGGGATGCCA CCTTCTGCTT CATCGTCTCG CTGGCGGTGG CTGATGTGGC
 26171 CGTGGGTGCG
 26172 181 CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT
 26173 CCACACCTGC
 26174 241 CTCATGGTTG CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC
 26175 CCTGCTGGCA
 26176 301 ATTGCTGTGG ACCGCTACCT CCGGGTCAAG ATCCCTCTCC GGTACAAGAT
 26177 GGTGGTGACC
 26178 361 CCCCCGGAGGG CGGCAGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT
 26179 GGTGGGACTG
 26180 421 ACCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGC
 26181 AGCCAACGGC
 26182 481 AGCATGGGG AGCCCGTGAT CAAGTGCAG TTCGAGAAGG TCATCAGCAT
 26183 GGAGTACATG
 26184 541 GTCTACTTCA ACTTCTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT
 26185 CCTCATCTAC
 26186 601 CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAAACAAGA AGGTGTGGC
 26187 CTCCTGGGC
 26188 661 GACCCGCAGA AGTACTATGG GAAGGAGCTG AAGATGCCA AGTCGCTGGC
 26189 CCTCATCTC
 26190 721 TTCCCTTTG CCCTCAGCTG GCTGCCTTG CACATCCTCA ACTGCATCAC
 26191 CCTCTCTGCG
 26192 781 CGTCCTGCC ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC
 26193 GCACGGCAAC
 26194 841 TCGGCCATGA ACCCCATTGT CTATGCCTTC CGCATCCAGA AGTTCCGGT
 26195 CACCTTCCTT
 26196 901 AAGATTTGGA ATGACCATTT CCGCTGCCAG CCTGCACCTC CCATTGACGA
 26197 GGATCCTCCA
 26198 961 AAAGAGAGGC CTGATGACTA G

26200 (2) INFORMATION FOR SEQ ID NO:2421:
 26201 (i) SEQUENCE CHARACTERISTICS:
 --> 26202 (A) LENGTH: 2900 base pairs
 26203 (B) TYPE: nucleic acid
 26204 (C) STRANDEDNESS: single
 26205 (D) TOPOLOGY: linear
 26206 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:
 26207 1 ATGAGTGTCA GAAGTGTGAA GGGTGCCTGT TCTGAATCCC AGAGCCTCCT

? what format
is this?
60
120

Cumulative
base totals,
per sequence
Run, seed
to be at
right margin
of each line

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:08

INPUT SET: S35381.raw

26208 CTCCCTCTGT
26209 61 GAGGCTGGCA GGTGAGGAAG GTTTAACCT CACTGGAAGG AATCCCTGGA
26210 GCTAGCGGCT
26211 121 GCTGAAGGCG TCGAGGTGTG GGGGCACTTG GACAGAACAG TCAGGCAGCC
26212 GGGAGCTCTG
26213 181 CCAGCTTG TGACCTTGGG CGGGCCTGGG AGCGCTGCGG CGGGAGCCGG
26214 AGGACTATGA
26215 241 GCTGCCGCGC GTTGTCCAGA GCCCAGCCA GCCCTACGCG CGCGGCCCCGG
26216 AGCTCTGTT
26217 301 CCTGGAACCTT TGGGCACTGC CTCTGGGACC CCTGCCGGCC AGCAGGCAGG
26218 ATGGTGTGTTG
26219 361 CCTCGTGCCTT CTTGGTGCCTT GTCTGCTGAT GTGCCAGCC TGTGCCCGCC
26220 ATGCCGCCCT
26221 421 CCATCTCAGC TTTCCAGGCC GCCTACATCG GCATCGAGGT GCTCATCGCC
26222 CTGGTCTCTG
26223 481 TGCCCGGGAA CGTGCTGGTG ATCTGGCGG TGAAGGTGAA CCAGGCCTG
26224 CGGGATGCCA
26225 541 CCTTCTGCTT CATCGTGTGCG CTGGCGGTGG CTGATGTGCC CGTGGGTGCC
26226 CTGGTCATCC
26227 601 CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT CCACACCTGC
26228 CTCATGGTTG
26229 661 CCTGTCCGGT CCTCATCCTC ACCCAGAGCT CCATCCTGGC CCTGCTGGCA
26230 ATTGCTGTGG
26231 721 ACCGCTACCT CCGGGTCAAG ATCCCCTCTCC GGTACAAGAT GGTGGTGACC
26232 CCCCGGGAGGG
26233 781 CGGCCTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT GGTGGGACTG
26234 ACCCCTATGT
26235 841 TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGC AGCCAACGGC
26236 AGCATGGGGG
26237 901 AGCCCGTGTGAT CAAGTGCAG TTGAGAAGG TCATCAGCAT GGAGTACATG
26238 GTCTACTTCA
26239 961 ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT CCTCATCTAC
26240 CTGGAGGTCT
26241 1021 TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC CTCCTCCGGC
26242 GACCCGCAGA
26243 1081 AGTACTATGG GAAGGAGCTG AAGATGCCA AGTCGCTGGC CCTCATCCTC
26244 TTCCTCTTTG
26245 1141 CCCTCAGCTG GCTGCCCTTG CACATCCTCA ACTGCATCAC CCTCTTCCTGC
26246 CCGTCCTGCC
26247 1201 ACAAGCCCAG CATCCTTACC TACATTGCCA TCTTCCTCAC GCACGGCAAC
26248 TCGGCCATGA
26249 1261 ACCCCATTGT CTATGCCCTC CGCATCCAGA AGTTCCGGT CACCTTCCTT
26250 AAGATTTGGA
26251 1321 ATGACCATTG CCGCTGCCAG CCTGCACCTC CCATTGACGA GGATCTCCCA
26252 GAAGAGAGGC
26253 1381 CTGATGACTA GACCCCGCCT TCCGCTCCA CCAGCCCACA TCCAGTGGGG
26254 TCTCAGTCCA
26255 1441 GTCCCTCACAT GCCCGCTGTC CCAGGGGTCT CCCTGAGCCT GCCCCAGCTG
26256 GGCTGTTGGC
26257 1501 TGGGGGCATG GGGGAGGCTC TGAAGAGATA CCCACAGAGT GTGGTCCCTC
26258 CACTAGGAGT
26259 1561 TAACTACCCCT ACACCTCTGG GCCCTGCAGG AGGCCTGGGA GGGCAAGGGT
26260 CCTACGGAGG

*Dane
Dawn*

**RAW SEQUENCE LISTING
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INPUT SET: S35381.raw

26261 1621 GACCAGGTGT CTAGAGGCAA CAGTGTCTG AGCCCCCACC TGCTGACCA
 26262 TCCCCATGAGC
 26263 1681 AGTCCAGCGC TTCAGGGCTG GGCAGGTCTT GGGGAGGCTG AGACTGCAGA
 26264 GGAGGCCACCT
 26265 1741 GGGCTGGGAG AAGGTGCTTG GGCTTCTGCG GTGAGGCAGG GGAGTCTGCT
 26266 TGTCTTAGAT
 26267 1801 GTTGGTGGTG CAGCCCCAGG ACCAAGCTTA AGGAGAGGAG AGCATCTGCT
 26268 CTGAGACGGA
 26269 1861 TGGAAAGGAGA GAGGTTGAGG ATGCACTGGC CTGTTCTGTA GGAGAGACTG
 26270 GCCAGAGGCA
 26271 1921 GCTAAGGGGC AGGAATCAAG GAGCCTCCGT TCCCACCTCT GAGGACTCTG
 26272 GACCCCCAGGC
 26273 1981 CATACCAGGT GCTAGGGTGC CTGCTCTCCT TGCCCTGGGC CAGCCCAGGA
 26274 TTGTACGTGG
 26275 2041 GAGAGGCAGA AAGGGTAGGT TCAGTAATCA TTTCTGATGA TTTGCTGGAG
 26276 TGCTGGCTCC
 26277 2101 ACGCCCTGGG GAGTGAGCTT GGTGCGGTAG GTGCTGGCCT CAAACAGCCA
 26278 CGAGGTGGTA
 26279 2161 GCTCTGAGCC CTCCTTCTTG CCCTGAGCTT TCCGGGGAGG AGCCTGGAGT
 26280 GTAATTACCT
 26281 2221 GTCATCTGGG CCACCAGCTC CACTGGCCCC CGTTGCCGGG CCTGGACTGT
 26282 CCTAGGTGAC
 26283 2281 CCCATCTCTG CTGCTTCTGG GCCTGATGGA GAGGAGAACCA CTAGACATGC
 26284 CAACTCGGGA
 26285 2341 GCATTCTGCC TGCCTGGAA CGGGGTGGAC GAGGGAGTGT CTGTAAGGAC
 26286 TCAGTGTGA
 26287 2401 CTGTAGGCAGC CCCTGGGGTG GGTTTAGCAG GCTGCAGCAG GCAGAGGAGG
 26288 AGTACCCCCC
 26289 2461 TGAGAGCATG TGGGGGAAGG CCTTGCTGTC ATGTGAATCC CTCAATACCC
 26290 CTAGTATCTG
 26291 2521 GCTGGGTTTT CAGGGGCTTT GGAAGCTCTG TTGCAGGTGT CCGGGGGTCT
 26292 AGGACTTTAG
 26293 2581 GGATCTGGGA TCTGGGAAG GACCAACCCA TGCCCTGCCA AGCCTGGAGC
 26294 CCCTGTGTTG
 26295 2641 GGGGGCAAGG TGGGGGAGCC TGGAGCCCC GTGTGGGAGG GCGAGGCCGG
 26296 GGAGCCTGGA
 26297 2701 GCCCCTGTGT GGGAGGGCGA GGCGGGGGAT CCTGGAGCCC CTGTGTCGGG
 26298 GGGCGAGGGA
 26299 2761 GGGGAGGTGG CCGTCGGTTG ACCTTCTGAA CATGAGTGTG AACTCCAGGA
 26300 CTTGCTTCCA
 26301 2821 AGCCCTTCCC TCTGTTGGAA ATTGGGTGTG CCCTGGCTCC CAAGGGAGGC
 26302 CCATGTGACT
 26303 2881 AATAAAAAAC TGTGAACCCCT
 26304

Done

Done

26305 (2) INFORMATION FOR SEQ ID NO:2422:
 26306 (i) SEQUENCE CHARACTERISTICS:
 --> 26307 (A) LENGTH: 1942 base pairs
 26308 (B) TYPE: nucleic acid
 26309 (C) STRANDEDNESS: single
 26310 (D) TOPOLOGY: linear
 26311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:
 26312 1 CGCATTGTG TTTTAATAAGAAGATCTGGA AGATAAAATAG TCTTGAAGAG

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679DATE: 04/25/2000
TIME: 12:29:09

INPUT SET: S35381.raw

26313 AGACAAAGGA
26314 61 AGGAAAATTT AAATCCTTAG ATTCAAGCAG AAGAATTCCA TGTGGAAGGT
26315 TTGGGTTGTT
26316 121 GTTGTGTTG TTTGGTGTGT TTTTTGTTT TTTGTTTTT TGTTTTTTT
26317 TGAGATGGAG
26318 181 TCTCGCTGTG TTACCGGGAG CGACAGAGCC GCACGGCCGA GTCGAGTCCC
26319 AGCCAGCTAC
26320 241 CATCCCTCTG GAGCTTACCG GCCGGCCTTG GCTTCCCCAG GAATCCCTGG
26321 AGCTAGCGGC
26322 301 TGCTGAAGGC GTCGAGGTGT GGGGGCACTT GGACAGAACAA GTCAGGCAGC
26323 CGGGAGCTCT
26324 361 GCCAGCTTG GTGACCTTGG GTGCTTGCT CGTCCCCCTT GGTGCCCGTC
26325 TGCTGATGTG
26326 421 CCCAGCCTGT GCCCGCCATG CCGCCCTCCA TCTCAGCTTT CCAGGCCGCC
26327 TACATCGGCA
26328 481 TCGAGGTGCT CATCGCCCTG GTCTCTGTGC CCGGGAACGT GCTGGTGATC
26329 TGGGCGGTGA
26330 541 AGGTGAACCCA GGCGCTGCAG GATGCCACCT TCTGCTTCAT CGTGTGCTG
26331 GCGGTGGCTG
26332 601 ATGTGCCCGT GGGTGCCCTG GTCATCCCCC TCGCCATCCT CATCAACATT
26333 GGGCCACAGA
26334 661 CCTACTTCCA CACCTGCCTC ATGGTTGCT GTCCGGTCCT CATCCTCAC
26335 CAGAGCTCCA
26336 721 TCCTGGCCCT GCTGGCAATT GCTGTGGACC GCTACCTCCG GGTCAAGATC
26337 CCTCTCCGGT
26338 781 ACAAGATGGT GGTGACCCCC CGGAGGGCGG CGGTGGCCAT AGCCGGCTGC
26339 TGGATCCTCT
26340 841 CCTTCGTGGT GGGACTGACC CCTATGTTG GCTGGAACAA TCTGAGTGCG
26341 GTGGAGCGGG
26342 901 CCTGGGCAGC CAACGGCAGC ATGGGGAGC CCGTGATCAA GTGGAGTT
26343 GAGAAGGTCA
26344 961 TCAGCATGGA GTACATGGTC TACTTCAACT TCTTTGTGTG GGTGCTGCC
26345 CCGCTTCTCC
26346 1021 TCATGGTCCT CATCTACCTG GAGGTCTTCT ACCTAATCCG CAAGCAGCTC
26347 AACAAAGAAGG
26348 1081 TGTCGGCCTC CTCCGGCAGC CCGCAGAAGT ACTATGGAA GGAGCTGAAG
26349 ATCGCCAAAGT
26350 1141 CGCTGGCCCT CATCCTCTTC CTCTTGCCCC TCAGCTGGCT GCCTTGCAC
26351 ATCCTCAACT
26352 1201 GCATCACCCCT CTTCTGCCCG TCCTGCCACA AGCCCAGCAT CCTTACCTAC
26353 ATTGCCATCT
26354 1261 TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA TGCCCTCCGC
26355 ATCCAGAAAGT
26356 1321 TCCCGTCAC CTTCCCTTAAG ATTTGGAATG ACCATTTCCG CTGCCAGCCT
26357 GCACCTCCCA
26358 1381 TTGACGAGGA TCTCCAGAA GAGAGGCCTG ATGACTAGAC CCCGCCTTCC
26359 GCTCCCCACCG
26360 1441 CCCACATCCA GTGGGGTCTC AGTCCAGTCC TCACATGCC GCTGTCCAG
26361 GGGTCTCCCT
26362 1501 GAGCCTGCC CAGCTGGCT GTTGGCTGG GGCATGGGG AGGCTCTGAA
26363 GAGATACCCA
26364 1561 CAGAGTGTGG TCCCTCCACT AGGAGTTAAC TACCCTACAC CTCTGGGCC
26365 TGCAGGAGGC

Dane

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679**

DATE: 04/25/2000
TIME: 12:29:09

INPUT SET: S35381.raw

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26366      1621 CTGGGAGGGC AAGGGTCCTA CGGAGGGACC AGGTGTCTAG AGGCAACAGT
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26368      1681 CCCACCTGCC TGACCATCCC ATGAGCAGTC CAGAGCTTCA GGGCTGGCA
26369      GGTCTGGGG
26370      1741 AGGCTGAGAC TGCAGAGGAG CCACCTGGC TGGGAGAAGG TGCTTGGCT
26371      TCTGCGGTGA
26372      1801 GGCAGGGAG TCTGCTTGTC TTAGATGTTG GTGGTGCAGC CCCAGGACCA
26373      AGCTTAAGGA
26374      1861 GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG TTGAGGATGC
26375      ACTGGCCTGT
26376      1921 TCTGTAGGAG AGACTGGCCA GA
26377

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*Please correct this type of error
in subsequent sequence?*

Name

26378 (2) INFORMATION FOR SEQ ID NO:2423:
 26379 (i) SEQUENCE CHARACTERISTICS:
 --> 26380 (A) LENGTH: 5904 base pairs
 26381 (B) TYPE: nucleic acid
 26382 (C) STRANDEDNESS: single
 26383 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

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26387 CCAGGGCGCTG CGGGATGCCA CCTTCTGCTT ATCGTCTCG CTGGCGGTGG CTGATGTGGC
26388 CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC ATTGGGCCAC AGACCTACTT
26389 CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCTC ACCCAGAGCT CCATCCTGGC
26390 CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CGGGGTCAAG ATCCCTCTCC GGTACAAGAT
26391 GGTGGTGACC CCCCAGGGGG CGGGGGTGGC CATAGCCGGC TGCTGGATCC TCTCCTTCGT
26392 GGTGGGACTG CCCCTATGT TTGGCTGGAA CAATCTGAGT GCGGTGGAGC GGGCCTGGC
26393 AGCCAACGGC AGCATGGGG AGCCCGTGT CAAGTGCAGG TTGAGAAGG TCATCAGCAT
26394 GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG CCCCCGCTTC TCCTCATGGT
26395 CCTCATCTAC CTGGAGGTCT TCTACCTAAT CCGCAAGCAG CTCAACAAGA AGGTGTCGGC
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26398 CCTCTCTGC CCGTCTGCC ACAAGCCAG CATCCTTAC TACATTGCCA TCTTCCTCAC
26399 GCACGGCAAC TCGGCCATGA ACCCATTGT CTATGCCCTC CGCATCCAGA AGTCCCGGT
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26403 GGTAAACCT CACTGGAAGG AATCCCTGGA GCTAGCGCT GCTGAAGGCG TCGAGGTGTG
26404 GGGGCACTTG GACAGAACAG TCAGGCAGCC GGGAGCTCTG CCAGCTTTGG TGACCTTGGG
26405 CCGGGCTGGG AGCGCTGCCG CGGGAGCCGG AGGACTATGA GCTGCCCGC GTTGTCCAGA
26406 GCCCAGCCCA GCCCTACCGC CGCGGCCCGG AGCTCTGTC CCTGGAACCT TGGGCACCTGC
26407 CTCTGGGACC CCTGCCGGCC AGCAGGCAGG ATGCTGCTTG CCTCGTGCCTC CTTGGTGCCTC
26408 GTCTGCTGAT GTGCCAGCC TGTGCCCGCC ATGCCGCCCT CCATCTCAGC TTTCCAGGCC
26409 GCCTACATCG GCATCGAGGT GCTCATCGCC CTGGTCTCTG TGCCCGGGAA CGTGTGGTG
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26411 CTGGCGGTGG CTGATGTGGC CGTGGGTGCC CTGGTCATCC CCCTCGCCAT CCTCATCAAC
26412 ATTGGGCCAC AGACCTACTT CCACACCTGC CTCATGGTTG CCTGTCCGGT CCTCATCCTC
26413 ACCCAGAGCT CCATCCTGGC CCTGCTGGCA ATTGCTGTGG ACCGCTACCT CGGGTCAAG
26414 ATCCCTCTCC GGTACAAGAT GGTGGTGACC CCCCAGGGGG CGGGGTGGC CATAGCCGGC
26415 TGCTGGATCC TCTCCTTCGT GGTGGGACTG ACCCCTATGT TTGGCTGGAA CAATCTGAGT
26416 GCGGTGGAGC GGGCCTGGC AGCCAACGGC AGCATGGGG AGCCCGTGT CAAGTGCAG
26417 TTCGAGAAGG TCATCAGCAT GGAGTACATG GTCTACTTCA ACTTCTTTGT GTGGGTGCTG

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*where
are
cumulative
last update?*

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/543,679**

DATE: 04/25/2000
TIME: 12:29:09

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26420	AAGATCGCCA	AGTCGCTGGC	CCTCATCCTC	TTCCTCTTG	CCCTCAGCTG	GCTGCCCTTG
26421	CACATCCTCA	ACTGCATCAC	CCTCTTCTGC	CCGTCCTGCC	ACAAGCCCAG	CATCCTTACC
26422	TACATTGCCA	TCTTCCTCAC	GCACGGCAAC	TCGGCCATGA	ACCCCATTGT	CTATGCCTTC
26423	CGCATCCAGA	AGTTCCCGGT	CACCTTCCCT	AAGATTGGA	ATGACCATT	CCGCTGCCAG
26424	CCTGCACCTC	CCATTGACGA	GGATCTCCC	GAAGAGAGGC	CTGATGACTA	GACCCGCCCT
26425	TCCGCTCCC	CCAGCCCACA	TCCAGTGGGG	TCTCAGTCCA	GTCCTCACAT	GCCCGCTGTC
26426	CCAGGGGTCT	CCCTGAGCCT	GCCCCAGCTG	GGCTGTTGGC	TGGGGGCATG	GGGGAGGCTC
26427	TGAAGAGATA	CCCACAGAGT	GTGGTCCCTC	CACTAGGAGT	TAACTACCC	ACACCTCTGG
26428	GCCCTGCAGG	AGGCCTGGGA	GGGCAAGGGT	CCTACGGAGG	GACCAGGTGT	CTAGAGGCAA
26429	CAGTGTCTG	AGCCCCCAC	TGCCTGACCA	TCCCATGAGC	AGTCCAGCGC	TTCAGGGCTG
26430	GGCAGGTCC	GGGGAGGCTG	AGACTGCAGA	GGAGCCACCT	GGGCTGGGAG	AAGGTGCTTG
26431	GGCTTCTGCG	GTGAGGGCAGG	GGAGTCTGCT	TGTCTTAGAT	GTTGGTGGTG	CAGCCCCAGG
26432	ACCAAGCTTA	AGGAGAGGAG	AGCATCTGCT	CTGAGACGGA	TGGAAGGAGA	GAGGTTGAGG
26433	ATGCACTGGC	CTGTTCTGTA	GGAGAGACTG	GCCAGAGGCA	GCTAAGGGGC	AGGAATCAAG
26434	GAGCCCTCGT	TCCCACCTCT	GAGGACTCTG	GACCCCAAGG	CATACCAGGT	GCTAGGGTGC
26435	CTGCTCTCCT	TGCCCCTGGGC	CAGCCCAGGA	TTGTACGTGG	GAGAGGCAGA	AAGGGTAGGT
26436	TCAGTAATCA	TTTCTGATGA	TTTGTCTGGAG	TGCTGGCTCC	ACGCCCTGGG	GAGTGAGCTT
26437	GGTGCCTGAG	GTGCTGGCT	CAAACAGCCA	CGAGGTGGTA	GCTCTGAGCC	CTCCTTCTTG
26438	CCCTGAGCTT	TCCGGGGAGG	AGCCTGGAGT	GTAATTACCT	GTCATCTGGG	CCACCAAGCTC
26439	CACTGGCCCC	CGTTGCCGGG	CCTGGACTGT	CCTAGGTGAC	CCCATCTCTG	CTGCTTCTGG
26440	GCCTGATGGA	GAGGAGAAC	CTAGACATGC	CAACTCGGG	GCATTCTGCC	TGCCTGGGAA
26441	CGGGGTGGAC	GAGGGAGTGT	CTGTAAGGAC	TCAGTGTGA	CTGTAGGCAGC	CCCTGGGGTG
26442	GGTTTAGCAG	GCTGCAGCAG	GCAGAGGAGG	AGTACCCCC	TGAGAGCATG	TGGGGGAAGG
26443	CCTTGTGTC	ATGTGAATCC	CTCAATACCC	CTAGTATCTG	GCTGGGTTTT	CAGGGCTTT
26444	GGAAGCTCTG	TTGCAGGTGT	CCGGGGGTCT	AGGACTTTAG	GGATCTGGGA	TCTGGGAAG
26445	GACCAACCCA	TGCCCCTGCCA	AGCCTGGAGC	CCCTGTGTTG	GGGGCAAGG	TGGGGGAGCC
26446	TGGAGCCCC	GTGTGGGAGG	GCGAGGCCGG	GGAGCCTGGA	GCCCCCTGTGT	GGGAGGGCGA
26447	GGCGGGGAT	CCTGGAGCCC	CTGTGTCGGG	GGGCGAGGGA	GGGGAGGTGG	CCGTCGGTTG
26448	ACCTTCTGAA	CATGAGTGT	AACTCCAGGA	CTTGCTTCCA	AGCCCTTCCC	TCTGTTGAA
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26450	CGCATTGTG	TTTTAATAAA	AGAATCTGGA	AGATAAAATAG	TCTTGAAGAG	AGACAAAGGA
26451	AGGAAAATTT	AAATCCTTAG	ATTCAAGCAG	AAGAATTCCA	TGTGGAAGGT	TTGGGTGTT
26452	GTTGTGTTG	TTTGGTGTG	TTTTGTGTTT	TTTGTGTTT	TGTTTGTGTT	TGAGATGGAG
26453	TCTCGCTGTG	TTACCGGGAG	CGACAGAGCC	GCACGGCCGA	GTCGAGTCCC	AGCCAGCTAC
26454	CATCCCTCTG	GAGCTTACCG	GCCGGCCTTG	GCTTCCCCAG	GAATCCCTGG	AGCTAGGGC
26455	TGCTGAAGGC	CTCGAGGTGT	GGGGCACTT	GGACAGAAC	GTCAGGCAGC	CGGGGACCTCT
26456	GCCAGCTTG	GTGACCTTGG	GTGCTTGCCT	CGTCCCCCTT	GGTCCCCGTC	TGCTGATGTG
26457	CCCAGCTGT	GGCCGCCATG	CCGCCCTCCA	TCTCAGCTTT	CCAGGGCCGCC	TACATCGGCA
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26460	ATGTGCCGT	GGGTGCCCTG	GTCATCCCC	TCGCCATCCT	CATCAACATT	GGGCCACAGA
26461	CCTACTTCCA	CACCTGCC	ATGGTTGCC	GTCCGGTCT	CATCCTCACC	CAGAGCTCCA
26462	TCCTGCCCT	GCTGGCAATT	GCTGTGGACC	GCTACCTCCG	GGTCAAGATC	CCTCTCCGGT
26463	ACAAGATGGT	GGTGACCCCC	CGGAGGGCGG	CGGTGGCCAT	AGCCGGCTGC	TGGATCCTCT
26464	CCTTCGTGGT	GGGACTGACC	CCTATGTTTG	GCTGGAACAA	TCTGAGTGC	GTGGAGCGGG
26465	CCTGGGCAGC	CAACGGCAGC	ATGGGGGAGC	CCGTGATCAA	GTGCGAGTTC	GAGAAGGTCA
26466	TCAGCATGGA	GTACATGGTC	TACTTCAACT	TCTTGTGTTG	GGTGCTGCC	
26467	CCGCTCTCC	TCATGGTCT	CATCTACCTG	GAGGTCTTCT	ACCTAATCCG	
26468	CAAGCAGCTC	ACAAGAAGG	TGTGGCCCTC	CTCCGGCGAC	CCGCAGAAGT	ACTATGGAA
26469	GGAGCTGAAG	ATCGCCAAGT	CGCTGGCCCT	CATCCTCTTC	CTCTTGTGCCC	TCAGCTGGCT
26470	GCCTTGTGAC	ATCCTCAACT	GCATCACCC	CTTCTGCCCG	TCCTGCCACA	AGCCCAGCAT

**RAW SEQUENCE LISTING
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TIME: 12:29:10

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26471 CCTTACCTAC ATTGCCATCT TCCTCACGCA CGGCAACTCG GCCATGAACC CCATTGTCTA
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 26473 CTGCCAGCCT GCACCTCCC TTGACGAGGA TCTCCAGAA GAGAGGCCTG ATGACTAGAC
 26474 CCCGCCTTCC GCTCCCACCG CCCACATCCA GTGGGCTCTC AGTCCAGTCC TCACATGCC
 26475 GCTGTCCCAG GGGTCTCCCT GAGCCTGCC CAGCTGGCT GTTGGCTGGG GGCATGGGG
 26476 AGGCTCTGAA GAGATACCCA CAGAGTGTGG TCCCTCACT AGGAGTTAAC TACCTACAC
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 26479 GGGCTGGCA GGTCTGGGG AGGCTGAGAC TGCAGAGGAG CCACCTGGGC TGGGAGAAGG
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 26481 CCCAGGACCA AGCTTAAGGA GAGGAGAGCA TCTGCTCTGA GACGGATGGA AGGAGAGAGG
 26482 TTGAGGATGC ACTGGCCTGT TCTGTAGGAG AGACTGGCCA GA GAT GGA GGG CGG
 26483 CAT GCC GGG G CGG GTC GCC GG GGG CBC BGG C GGC GGG CBC GC GGC
 26484 CTG G GGB GGG CGG C GBT GGB GGG GG CTG GGC GC GGC CTG GAA AGC
 26485 TGA GAT GGA GGG CGG CAT GGC GGG CAC AGG CTG GGC
 26486

Name
Please correct the type of error for subsequent sequences

26487 (2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1687 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

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121 CCAGCTGGCC CGGCCATGCT GCTGGAGACA CAGGACGCGC TGTACGTGGC

GCTGGAGCTG

181 GTCATCGCCG CGCTTCGGT GGCGGGCAAC GTGCTGGTGT CGGCCGCGGT

GGGCACGGCG

241 AACACTCTGC AGACGCCAC CAACTACTTC CTGGTGTCCC TGGCTGCC

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301 GTGGGGCTCT TCGCCATCCC CTTTGCCATC ACCATCAGCC TGGGCTTCTG

CACTGACTTC

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601 GAACCTGGG ATGGAACCAC GAATGAAAGC TGCTGCCTTG TGAAGTGTCT

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661 GTGGTCCCCA TGAGCTACAT GGTATATTTC AATTCTTTG GGTGTGTTCT

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781 ACTGAGCTGA TGGACCACTC GAGGACCACTC CTCCAGCGGG AGATCCATGC

AGCCAAGTCA

841 CTGGCCATGA TTGTGGGAT TTTTGCCCTG TGCTGGTTAC CTGTGCATGC